

SEQUENCE LISTING

(1) GENERAL INFORMATION:

5 (i) APPLICANT:
 (A) NAME: Max-Planck-Gesellschaft zur Foerderung
 der
 Wissenschaften e.V.
 (B) STREET: Hofgartenstrasse 2
 10 (C) CITY: Muenchen
 (E) COUNTRY: Germany
 (F) POSTAL CODE (ZIP): 80539

(ii) TITLE OF INVENTION: Tuberculosis vaccine

15 (iii) NUMBER OF SEQUENCES: 2

(iv) COMPUTER READABLE FORM:
 (A) MEDIUM TYPE: Floppy disk
 20 (B) COMPUTER: IBM PC compatible
 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 (D) SOFTWARE: PatentIn Release #1.0, Version
 #1.30 (EPO)

25 (2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1881 base pairs
 (B) TYPE: nucleic acid
 30 (C) STRANDEDNESS: both
 (D) TOPOLOGY: linear

(ix) FEATURE:
 (A) NAME/KEY: CDS
 35 (B) LOCATION: 1..1878

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

40	ATG ACA GAC GTG AGC CGA AAG ATT CGA GCT TGG GGA CGC CGA TTG ATG	48
	Met Thr Asp Val Ser Arg Lys Ile Arg Ala Trp Gly Arg Arg Leu Met	
	1 5 10 15	
45	ATC GGC ACG GCA GCG GCT GTA GTC CTT CCG GGC CTG GTG GGG CTT GCC	96
	Ile Gly Thr Ala Ala Val Val Leu Pro Gly Leu Val Gly Leu Ala	
	20 25 30	
50	GGC GGA GCG GCA ACC GCG GGC GCG TTC TCC CGG CCG GGG CTG CCG GTC	144
	Gly Gly Ala Ala Thr Ala Gly Ala Phe Ser Arg Pro Gly Leu Pro Val	
	35 40 45	
55	GAG TAC CTG CAG TCT GCA AAG CAA TCC GCT GCA AAT AAA TTG CAC TCA	192
	Glu Tyr Leu Gln Ser Ala Lys Gln Ser Ala Ala Asn Lys Leu His Ser	
	50 55 60	
60	GCA GGA CAA AGC ACG AAA GAT GCA TCT GCA TTC AAT AAA GAA AAT TCA	240
	Ala Gly Gln Ser Thr Lys Asp Ala Ser Ala Phe Asn Lys Glu Asn Ser	
	65 70 75 80	
60	ATT TCA TCC ATG GCA CCA CCA GCA TCT CCG CCT GCA AGT CCT AAG ACG	288
	Ile Ser Ser Met Ala Pro Pro Ala Ser Pro Pro Ala Ser Pro Lys Thr	
	85 90 95	

	CCA ATC GAA AAG AAA CAC GCG GAT GAA ATC GAT AAG TAT ATA CAA GGA Pro Ile Glu Lys Lys His Ala Asp Glu Ile Asp Lys Tyr Ile Gln Gly 100 105 110	336
5	TTG GAT TAC AAT AAA AAC AAT GTA TTA GTA TAC CAC GGA GAT GCA GTG Leu Asp Tyr Asn Lys Asn Asn Val Leu Val Tyr His Gly Asp Ala Val 115 120 125	384
10	ACA AAT GTG CCG CCA AGA AAA GGT TAC AAA GAT GGA AAT GAA TAT ATT Thr Asn Val Pro Pro Arg Lys Gly Tyr Lys Asp Gly Asn Glu Tyr Ile 130 135 140	432
15	GTT GTG GAG AAA AAG AAG AAA TCC ATC AAT CAA AAT AAT GCA GAC ATT Val Val Glu Lys Lys Lys Lys Ser Ile Asn Gln Asn Asn Ala Asp Ile 145 150 155 160	480
20	CAA GTT GTG AAT GCA ATT TCG AGC CTA ACC TAT CCA GGT GCT CTC GTA Gln Val Val Asn Ala Ile Ser Ser Leu Thr Tyr Pro Gly Ala Leu Val 165 170 175	528
25	AAA GCG AAT TCG GAA TTA GTA GAA AAT CAA CCA GAT GTT CTC CCT GTA Lys Ala Asn Ser Glu Leu Val Glu Asn Gln Pro Asp Val Leu Pro Val 180 185 190	576
30	AAA CGT GAT TCA TTA ACA CTC AGC ATT GAT TTG CCA GGT ATG ACT AAT Lys Arg Asp Ser Leu Thr Leu Ser Ile Asp Leu Pro Gly Met Thr Asn 195 200 205	624
35	CAA GAC AAT AAA ATC GTT GTA AAA AAT GCC ACT AAA TCA AAC GTT AAC Gln Asp Asn Lys Ile Val Val Lys Asn Ala Thr Lys Ser Asn Val Asn 210 215 220	672
40	AAC GCA GTA AAT ACA TTA GTG GAA AGA TGG AAT GAA AAA TAT GCT CAA Asn Ala Val Asn Thr Leu Val Glu Arg Trp Asn Glu Lys Tyr Ala Gln 225 230 235 240	720
45	GCT TAT CCA AAT GTA AGT GCA AAA ATT GAT TAT GAT GAC GAA ATG GCT Ala Tyr Pro Asn Val Ser Ala Lys Ile Asp Tyr Asp Asp Glu Met Ala 245 250 255	768
50	TAC AGT GAA TCA CAA TTA ATT GCG AAA TTT GGT ACA GCA TTT AAA GCT Tyr Ser Glu Ser Gln Leu Ile Ala Lys Phe Gly Thr Ala Phe Lys Ala 260 265 270	816
55	GTA AAT AAT AGC TTG AAT GTA AAC TTC GGC GCA ATC AGT GAA GGG AAA Val Asn Asn Ser Leu Asn Val Asn Phe Gly Ala Ile Ser Glu Gly Lys 275 280 285	864
60	ATG CAA GAA GAA GTC ATT AGT TTT AAA CAA ATT TAC TAT AAC GTG AAT Met Gln Glu Glu Val Ile Ser Phe Lys Gln Ile Tyr Tyr Asn Val Asn 290 295 300	912
65	GTT AAT GAA CCT ACA AGA CCT TCC AGA TTT TTC GGC AAA GCT GTT ACT Val Asn Glu Pro Thr Arg Pro Ser Arg Phe Phe Gly Lys Ala Val Thr 305 310 315 320	960
70	AAA GAG CAG TTG CAA GCG CTT GGA GTG AAT GCA GAA AAT CCT CCT GCA Lys Glu Gln Leu Gln Ala Leu Gly Val Asn Ala Glu Asn Pro Pro Ala 325 330 335	1008
75	TAT ATC TCA AGT GTG GCG TAT GGC CGT CAA GTT TAT TTG AAA TTA TCA Tyr Ile Ser Ser Val Ala Tyr Gly Arg Gln Val Tyr Leu Lys Leu Ser 340 345 350	1056
80	ACT AAT TCC CAT AGT ACT AAA GTA AAA GCT GCT TTT GAT GCT GCC GTA Thr Asn Ser His Ser Thr Lys Val Lys Ala Ala Phe Asp Ala Ala Val 355 360 365	1104
85	AGC GGA AAA TCT GTC TCA GGT GAT GTA GAA CTA ACA AAT ATC ATC AAA Ser Gly Lys Ser Val Ser Gly Asp Val Glu Leu Thr Asn Ile Ile Lys 370 375 380	1152

	AAT TCT TCC TTC AAA GCC GTA ATT TAC GGA GGT TCC GCA AAA GAT GAA	1200
	Asn Ser Ser Phe Lys Ala Val Ile Tyr Gly Gly Ser Ala Lys Asp Glu	
	385 390 395 400	
5	GTT CAA ATC ATC GAC GGC AAC CTC GGA GAC TTA CGC GAT ATT TTG AAA	1248
	Val Gln Ile Ile Asp Gly Asn Leu Gly Asp Leu Arg Asp Ile Leu Lys	
	405 410 415	
10	AAA GGC GCT ACT TTT AAT CGA GAA ACA CCA GGA GTT CCC ATT GCT TAT	1296
	Lys Gly Ala Thr Phe Asn Arg Glu Thr Pro Gly Val Pro Ile Ala Tyr	
	420 425 430	
15	ACA ACA AAC TTC CTA AAA GAC AAT GAA TTA GCT GTT ATT AAA AAC AAC	1344
	Thr Thr Asn Phe Leu Lys Asp Asn Glu Leu Ala Val Ile Lys Asn Asn	
	435 440 445	
20	TCA GAA TAT ATT GAA ACA ACT TCA AAA GCT TAT ACA GAT GGA AAA ATT	1392
	Ser Glu Tyr Ile Glu Thr Thr Ser Lys Ala Tyr Thr Asp Gly Lys Ile	
	450 455 460	
25	AAC ATC GAT CAC TCT GGA GGA TAC GTT GCT CAA TTC AAC ATT TCT TGG	1440
	Asn Ile Asp His Ser Gly Gly Tyr Val Ala Gln Phe Asn Ile Ser Trp	
	465 470 475 480	
30	GAT GAA GTA AAT TAT GAT CCT GAA GGT AAC GAA ATT GTT CAA CAT AAA	1488
	Asp Glu Val Asn Tyr Asp Pro Glu Gly Asn Glu Ile Val Gln His Lys	
	485 490 495	
35	AAC TGG AGC GAA AAC AAT AAA AGC AAG CTA GCT CAT TTC ACA TCG TCC	1536
	Asn Trp Ser Glu Asn Asn Lys Ser Lys Leu Ala His Phe Thr Ser Ser	
	500 505 510	
40	ATC TAT TTG CCA GGT AAC GCG AGA AAT ATT AAT GTT TAC GCT AAA GAA	1584
	Ile Tyr Leu Pro Gly Asn Ala Arg Asn Ile Asn Val Tyr Ala Lys Glu	
	515 520 525	
45	TGC ACT GGT TTA GCT TGG GAA TGG TGG AGA ACG GTA ATT GAT GAC CGG	1632
	Cys Thr Gly Leu Ala Trp Glu Trp Trp Arg Thr Val Ile Asp Asp Arg	
	530 535 540	
50	AAC TTA CCA CTT GTG AAA AAT AGA AAT ATC TCC ATC TGG GGC ACC ACG	1680
	Asn Leu Pro Leu Val Lys Asn Arg Asn Ile Ser Ile Trp Gly Thr Thr	
	545 550 555 560	
55	CTT TAT CCG AAA TAT AGT AAT AAA GTA GAT AAT CCA ATC GAA TAT GCA	1728
	Leu Tyr Pro Lys Tyr Ser Asn Lys Val Asp Asn Pro Ile Glu Tyr Ala	
	565 570 575	
60	TTA GCC TAT GGA AGT CAG GGT GAT CTT AAT CCA TTA ATT AAT GAA ATC	1776
	Leu Ala Tyr Gly Ser Gln Gly Asp Leu Asn Pro Leu Ile Asn Glu Ile	
	580 585 590	
65	AGC AAA ATC ATT TCA GCT GCA GTT CTT TCC TCT TTA ACA TCG AAG CTA	1824
	Ser Lys Ile Ile Ser Ala Ala Val Leu Ser Ser Leu Thr Ser Lys Leu	
	595 600 605	
70	CCT GCA GAG TTC GTT AGG CGC GGA TCC GGA ATT CGA AGC TTA TCG ATG	1872
	Pro Ala Glu Phe Val Arg Arg Gly Ser Gly Ile Arg Ser Leu Ser Met	
	610 615 620	
75	TCG ACG TAG	1881
	Ser Thr	
	625	

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 626 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

10 Met Thr Asp Val Ser Arg Lys Ile Arg Ala Trp Gly Arg Arg Leu Met
 1 5 10 15
 15 Ile Gly Thr Ala Ala Ala Val Val Leu Pro Gly Leu Val Gly Leu Ala
 20 25 30
 Gly Gly Ala Ala Thr Ala Gly Ala Phe Ser Arg Pro Gly Leu Pro Val
 35 40 45
 20 Glu Tyr Leu Gln Ser Ala Lys Gln Ser Ala Ala Asn Lys Leu His Ser
 50 55 60
 25 Ala Gly Gln Ser Thr Lys Asp Ala Ser Ala Phe Asn Lys Glu Asn Ser
 65 70 75 80
 Ile Ser Ser Met Ala Pro Pro Ala Ser Pro Pro Ala Ser Pro Lys Thr
 85 90 95
 30 Pro Ile Glu Lys Lys His Ala Asp Glu Ile Asp Lys Tyr Ile Gln Gly
 100 105 110
 Leu Asp Tyr Asn Lys Asn Asn Val Leu Val Tyr His Gly Asp Ala Val
 115 120 125
 35 Thr Asn Val Pro Pro Arg Lys Gly Tyr Lys Asp Gly Asn Glu Tyr Ile
 130 135 140
 Val Val Glu Lys Lys Lys Lys Ser Ile Asn Gln Asn Asn Ala Asp Ile
 145 150 155 160
 40 Gln Val Val Asn Ala Ile Ser Ser Leu Thr Tyr Pro Gly Ala Leu Val
 165 170 175
 Lys Ala Asn Ser Glu Leu Val Glu Asn Gln Pro Asp Val Leu Pro Val
 180 185 190
 45 Lys Arg Asp Ser Leu Thr Leu Ser Ile Asp Leu Pro Gly Met Thr Asn
 195 200 205
 50 Gln Asp Asn Lys Ile Val Val Lys Asn Ala Thr Lys Ser Asn Val Asn
 210 215 220
 Asn Ala Val Asn Thr Leu Val Glu Arg Trp Asn Glu Lys Tyr Ala Gln
 225 230 235 240
 55 Ala Tyr Pro Asn Val Ser Ala Lys Ile Asp Tyr Asp Asp Glu Met Ala
 245 250 255
 Tyr Ser Glu Ser Gln Leu Ile Ala Lys Phe Gly Thr Ala Phe Lys Ala
 260 265 270
 60 Val Asn Asn Ser Leu Asn Val Asn Phe Gly Ala Ile Ser Glu Gly Lys
 275 280 285
 65 Met Gln Glu Glu Val Ile Ser Phe Lys Gln Ile Tyr Tyr Asn Val Asn
 290 295 300
 Val Asn Glu Pro Thr Arg Pro Ser Arg Phe Phe Gly Lys Ala Val Thr
 305 310 315 320
 70 Lys Glu Gln Leu Gln Ala Leu Gly Val Asn Ala Glu Asn Pro Pro Ala
 325 330 335

Tyr Ile Ser Ser Val Ala Tyr Gly Arg Gln Val Tyr Leu Lys Leu Ser
 340 345 350
 5 Thr Asn Ser His Ser Thr Lys Val Lys Ala Ala Phe Asp Ala Ala Val
 355 360 365
 Ser Gly Lys Ser Val Ser Gly Asp Val Glu Leu Thr Asn Ile Ile Lys
 370 375 380
 10 Asn Ser Ser Phe Lys Ala Val Ile Tyr Gly Gly Ser Ala Lys Asp Glu
 385 390 395 400
 Val Gln Ile Ile Asp Gly Asn Leu Gly Asp Leu Arg Asp Ile Leu Lys
 405 410 415
 15 Lys Gly Ala Thr Phe Asn Arg Glu Thr Pro Gly Val Pro Ile Ala Tyr
 420 425 430
 Thr Thr Asn Phe Leu Lys Asp Asn Glu Leu Ala Val Ile Lys Asn Asn
 435 440 445
 20 Ser Glu Tyr Ile Glu Thr Thr Ser Lys Ala Tyr Thr Asp Gly Lys Ile
 450 455 460
 25 Asn Ile Asp His Ser Gly Gly Tyr Val Ala Gln Phe Asn Ile Ser Trp
 465 470 475 480
 Asp Glu Val Asn Tyr Asp Pro Glu Gly Asn Glu Ile Val Gln His Lys
 485 490 495
 30 Asn Trp Ser Glu Asn Asn Lys Ser Lys Leu Ala His Phe Thr Ser Ser
 500 505 510
 35 Ile Tyr Leu Pro Gly Asn Ala Arg Asn Ile Asn Val Tyr Ala Lys Glu
 515 520 525
 Cys Thr Gly Leu Ala Trp Glu Trp Trp Arg Thr Val Ile Asp Asp Arg
 530 535 540
 40 Asn Leu Pro Leu Val Lys Asn Arg Asn Ile Ser Ile Trp Gly Thr Thr
 545 550 555 560
 Leu Tyr Pro Lys Tyr Ser Asn Lys Val Asp Asn Pro Ile Glu Tyr Ala
 565 570 575
 45 Leu Ala Tyr Gly Ser Gln Gly Asp Leu Asn Pro Leu Ile Asn Glu Ile
 580 585 590
 50 Ser Lys Ile Ile Ser Ala Ala Val Leu Ser Ser Leu Thr Ser Lys Leu
 595 600 605
 Pro Ala Glu Phe Val Arg Arg Gly Ser Gly Ile Arg Ser Leu Ser Met
 610 615 620
 55 Ser Thr
 625